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Leu Lys Ala Ala Met Gln Glu Ala Arg Gly Leu Gln Phe Val Trp Arg
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Gly Ser Pro Ser Leu Ser Glu Arg Gln Glu Ile Phe Thr His Ile Met
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Asp Gln Tyr Ser Tyr Cys Thr Pro Ser His Ile Pro Phe Ser Asn Arg
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Ser Gly Phe Tyr Trp Asn Gly Val Ala Val Phe Pro Lys Pro Pro
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Asp Gly Val Tyr Pro Asn Met Ser Glu Pro Val Thr Pro Ala Asn Ile
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 Asn Leu Tyr Ala Glu Ala Leu Val Ala Asn Val Lys Gln Arg Ala Ala
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 Trp Phe Arg Thr Pro His Val Leu Trp Pro Trp Gly Cys Asp Lys Gln
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 Phe Phe Asn Ala Ser Val Gln Phe Ala Asn Met Asp Pro Leu Leu Asp
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Gln	Ala	Trp	Thr	Gly	Phe	Tyr	Thr	Ser	Arg	Ser	Ser	Leu	Lys	Gly	Leu
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Ala	Arg	Arg	Ala	Ser	Ala	Leu	Leu	Tyr	Ala	Gly	Glu	Ser	Met	Phe	Thr
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Arg	Tyr.	Leu	Trp	Pro	Ala	Pro	Arg		His	Leu	Asp	Pro	Thr	Trp	Ala
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Leu	Gln		Leu	Gln	Gln	Leu	Arg	Trp	Ala	Val	Ser	GIU	vaı	GIN	HIS
		275					280		D	T	17-1	285	New.	Met	Tur
His	_	Ala	Ile	Thr	GIA		Glu	Ser	Pro	ьуs	300	Arg	wsb	MEL	ıyı
	290					295		T	C111	v-1		Tare	T.=11	Met	Δla
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Ser	IIe	vaı	Leu		GIU	neu	GIII	PIU	330	AIG	110			335	
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Ile	Pro	Gly	Leu	Ser	Tyr	Arg	His	Tyr	Ser	Ile	Arg	Pro	Thr	Ala	Gly
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Ala	Gln	Glụ	Gly	Thr	Gln	Glu	Pro		Ala	Thr	Val	Ala	Ser	Thr	Leu
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Gln	Phe		Arg	Arg	Leu	Arg	Arg	Arg	Thr	Ser	HIS	Ala	GIY	Arg	IYL
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Val	Thr	Glu	Ile	Arg	Gln	Tyr	Phe	Tyr	Arg	Asn	Met	Thr	Ala	Gln	Asn
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Tyr	Thr	Tyr	Ala	Ile	Arg	Ser	Arg	Leu	Thr	His	Val	Pro	Gln	Gly	His
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Asn	Ser	Gln	Gln	Val	Ile	TYT	ser	Asp	ASD	LASI	, сту	TAI	GID	יייפני	Gln

595

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Tyr Pro Met Val Gln Ser Ala Phe Met Glu Asp Gly Lys Ser Arg Leu
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Asp Leu Ala Gly Thr Ala Pro Lys Leu Pro Gly Pro Gln Gln Gln Glu
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Ala Val Thr Leu Pro Pro Asn Leu His Leu Gln Ile Leu Ser Ile Pro
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Gly Trp Arg Tyr Ser Ser Asn His Thr Glu His Ser Gln Asn Leu Arg
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Lys Gly His Arg Gly Glu Ala Gln Ala Asp Leu Arg Arg Val Leu Leu
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Arg Leu Tyr His Leu Tyr Glu Val Gly Glu Asp Pro Val Leu Ser Gln
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Ser Ala Ile Glu Ala Met Lys Lys Ala Tyr Gln Glu Glu Leu Ser Arg
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Glu Leu Ser Lys Thr Arg Ser Leu Gln Gln Gly Pro Asp Gly Leu Arg
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Lys Gln His Gln Ser Asp Val Glu Ala Leu Lys Arg Glu Leu Gln Val
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                                                     110
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                             120
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Glu Glu Ile Asp Gln Leu Arg Gly Phe Ile Ala Ser Gln Gly Met Gly
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Asn Gly Cys Gly Arg Ser Asn Glu Arg Ser Ser Cys Glu Leu Glu Val
                                     170
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Leu Leu Arg Val Lys Glu Asn Glu Leu Gln Tyr Leu Lys Lys Glu Val
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                                 185
Gln Cys Leu Arg Asp Glu Leu Gln Met Met Gln Lys Asp Lys Arg Phe
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Thr Ser Gly Lys Tyr Gln Asp Val Tyr Val Glu Leu Ser His Ile Lys
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215
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Thr Arg Ser Glu Arg Glu Ile Glu Gln Leu Lys Glu His Leu Arg Leu
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840

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1140				aactccaccc	
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2040				ttcacattgc	
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2220					aaataggaaa
2280				•	gtectgcacg
2340				•	ataatcggat
2400					cgtccatttg
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cettgcacce aagtcagttg atgtcatcat agatgctggg cgtcgggggt geeggtgget
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Cys Thr Gln Thr Gly His Ala Gln Pro Cys Pro Ser Ala Pro Ser Thr
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Gly Pro Ile His Ile Ala Glu Gly Gly Arg Gly Arg Pro Pro Pro Gly
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Ser Ala Ser Asn Pro Gln Pro Pro Gly Ser Pro His Cys Pro Ser Ala
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Gly Leu Ser Pro Val Pro Gly Val Gly Gly Arg Gln Cys Pro Gly Thr
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                                     90
Val Pro Arg Val Arg Arg Pro Gly Leu Ala Gly His Pro Val Thr His
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Arg Ile Asn Arg Lys Thr Ala Ser Pro Pro Asn Leu Cys Pro Arg His
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Thr Pro Ser Gly Arg Ser Gly Pro Ala Ala Pro Trp Arg Thr Pro Ala
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120

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Thr Leu Gln Gln Arg Val Phe Gln Ile Leu Asp Ser Lys Leu Phe Glu
Lys Val Lys Glu Val Cys Pro Asn Val His Glu Lys Ile Arg Ala Ile
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Tyr Ala Asp Leu Asn Gln Asn Asp Phe Ala Ile Ser Lys Glu Asp Met
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Gln Glu Leu Leu Ser Cys Thr Asn Ile Ile Phe His Cys Ala Ala Thr
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Val Arg Phe Asp Asp Thr Leu Arg His Ala Val Gln Leu Asn Val Thr
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Ala Thr Arg Gln Leu Leu Leu Met Ala Ser Gln Met Pro Lys Leu Glu
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Ala Phe Ile His Ile Ser Thr Ala Tyr Ser Asn Cys Asn Leu Lys His
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Asp Val Ile Pro Val Asp Thr Val Val Asn Leu Met Leu Ala Val Gly
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Trp Tyr Thr Ala Val His Arg Pro Lys Ser Thr Leu Val Tyr His Ile
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Val Leu Ala Thr Phe Glu Lys Ile Pro Phe Glu Arg Pro Phe Arg Arg
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Leu Thr Gly Arg Lys Pro Arg Met Thr Lys Leu Met Asn Arg Leu Leu
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375

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370

380

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Leu Ile Ala Arg Ser Gln Met Ala Arg Asn Val Trp Phe Phe Ile Val
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Phe Val Leu Pro Thr Glu Gln Phe His Leu Gly Lys Ile Glu Glu Leu
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Leu His Pro Ala Val Val Lys Pro His Leu Gly His Val Pro Asp Tyr
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Val Thr Ser Gly Leu Thr Tyr Ile Lys Ile Gln Leu Val Lys Ala Glu
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Val Ala Ser Ala Val Cys Leu Arg Leu His Arg Pro Arg Asp Ala Ser
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65	_		_	_	70		_			75					80
Thr	Leu	GIA	Leu		Gln	Ile	Lys	Leu		Gly	Leu	Thr	Ala		Gly
-		_	_	85			_	_	90		_	_	_	95	
Thr	Thr	ser		Ala	Thr	Vai	Asn			Phe	Leu	Pro		GLu	Asp
~1	**- 1		100	m1		- 2 -	~1	105		_		-	110		~
GIN	vaı		гÀг	Inr	ser	ire	Gly	Trp	Leu	Arg	Leu		His	HlS	Cys
T	m\	115	-1 -			.	120	~1				125			
Leu	130	HIS	iie	ser	Asp		Glu	GIY	Met	Met		ser	Ala	ATA	Ala
Dwa		27.	7	T	T 0	135	Thr		7.1 - -	21-	140	*	W- h	C	D
145	1111	MIG	WPII	neu	150	GIII	1111	Cys	Ala	155	ьeu	Leu	Mec	ser	160
	Cve	Glaz	Met	Hie		Pro	Asn	Tla	Glu		v-1	T.All	Val	Tare	
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Glv	Leu	Gln	Ser		Ara	Ile	Glv	Leu		Leu	Tle	Asp	Tle		Leu
1			180		5		U-1	185	-,-				190		
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Ĭ		195				•	200					205			
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305	на	пец	Leu	ASP	310	GIU	Leu	PHE	Gru	315	Leu	PILE	ASII	пр	320
	Ser	ī.eu	Pro	Cvs		Met	Val	T.e.ii	Lve		Δla	Val	Aen	Sar	
	001	20 u		325	7011		V		330	Lys	714	Val	AJP	335	Deu
Leu	Cvs	Ser	Met		His	Val	His	Pro		Tvr	Phe	Ser	Leu		Met
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3		435	71 -	3	T	.	440		***	*** -	**- 3	445	~1	a1 -	
ASP	450	ser	GIN	ASP	гÀг		Arg	Arg	nis	nıs		PTO	GIN	GID	cys
7.00		Mo+	Dro	T7 ^	Th~	455	7	T 633	17-7	הוה	460	T1 ^	T 011	A	Dha
465	nys	MEC	FIU	116	470	Ara	Asp	nen	val	475	FIO	TTE	nen	ντά	480
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				485					490	-13				495	y
Ser	Glu	Val	Asn		Leu	Trp	Thr	Ala		Leu	Phe	Leu	Leu		His
						-								•	

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Tyr Ala Glu Val			Glu Ara	_		Gln	Cvs	T.e.11	_
172 014 .44.	965	ביים כיים	ora mra	970	u	01	Cyo	975	200
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1370

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1365

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Ser Ser His Ser Pro Thr Ser Ala Ser Gln Ala Val Gly Thr Thr Gly
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Glu Glu Arg Gln Gln His Gly Glu Cys Pro Val Pro Thr Pro Trp Lys
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Phe Val Phe Thr Tyr Lys Gly Leu Arg Ala Leu Gln Ser Tyr Ile Gln
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Thr Leu Gln Pro Ser Leu Gln Ser Ser Met Thr Tyr Leu Tyr Glu Asp
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Pro Leu Leu Pro Gly Ser Leu Asp Leu Pro Glu Leu Gln Pro Ala Ala
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Thr Phe Val Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe
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Trp Thr Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val
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Phe Phe Pro . Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp Leu
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Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val Leu Arg
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Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr Leu Gly Val
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Leu Glu Val Gly Cys Gly Val Gly Asn Thr Val Phe Pro Ile Leu Gln
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Thr Ala Ile Glu Leu Val Gln Thr Asn Ser Glu Tyr Asp Pro Ser Arg
Cys Phe Ala Phe Val His Asp Leu Cys Asp Glu Glu Lys Ser Tyr Pro
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Val Pro Lys Gly Ser Leu Asp Ile Ile Ile Leu Ile Phe Val Leu Ser
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Ala Ile Val Pro Asp Lys Met Gln Lys Ala Ile Asn Arg Leu Ser Arg
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Phe Tyr Val Arg Gly Asp Gly Thr Arg Val Tyr Phe Phe Thr Gln Glu
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Glu Leu Asp Thr Leu Phe Thr Thr Ala Gly Leu Glu Lys Val Gln Asn
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Leu Val Asp Arg Arg Leu Gln Val Asn Arg Gly Lys Gln Leu Thr Met
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Asn Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala Asp Gly Val Ser
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Tyr Ala Cys Lys Asp Leu Gly Ala Asp Ile Ile Leu Asp Met Ala Thr
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Phe		Gln	Leu	Tle	Phe		Thr	Va 1	Hie	Glv		Tvr	Tare	Aen	7~~
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	Ala	Tvr	Arg	Asn		Met	Thr	Acn	Va 1		17-1	Gln	uie	Tan	
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Thr	Glu	Gln	Lys		Δτα	Tla	Lare	Cve		GI.	Tan	7/27	Ture		T1 o
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	Cvs	T.e.13	His	Va 1		Ser	בוד	Ser	λla		C1.,	17-1	חדם	C1-	
	٠,٥			565	1110	JCI	116	Jei	570	val	Gru	Val	PIO		Ser
בומ	Dro	Met	Tyr		Тъгъ	LAII	7 cm	7 ~~		T 0	Dho	T	~1··	575	П
AIG	110	1100	580	GIII	171	neu	nsp	585	пåа	neu	Pne	ьys		Ата	Tyr
Gln	т1а	ת ו ת		T 011	Gl v	V-1	mb	-	mL	n	m	3	590	• • • •	
GLII	110	595	Cys	Deu	Gry	vai		ASD	IIIL	Asp	irp		GIU	ьeu	Ala
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Tla		17 = 1	G1 ~	7 c-	Len	615	The	T	~ 1	T	620		C -	- 3	-1
625	AT A	AGT	Gln	лър	630	wrg	ıyr	neu	ĢΙU		тте	ser	ser	тте	
	h ~~	tara	Tare	7~~		C1	mb	n	n	635	T	DL -	.		640
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Ile Ser Asn Asn Ser Lys Leu Thr Ser His Ala Ile Thr Leu Gln Lys
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Thr Val Glu Tyr Ile Thr Lys Leu Gln Glu Arg Gly Gln Met Gln
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Glu Glu Ala Arg Arg Leu Arg Glu Glu Ile Glu Glu Leu Asn Ala Thr
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Ile Ile Ser Cys Gln Gln Leu Leu Pro Ala Thr Gly Val Pro Val Thr
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Arg Arg Gln Phe Asp His Met Lys Asp Met Phe Asp Glu Tyr Val Lys
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Lys Pro Leu Phe Glu Ser Phe Lys Gly Met Val Ser Thr Ser Ser Leu
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Leu Val Phe Gln Lys Asp Asp Gly Phe Asp Asn Leu Tyr Tyr Val Thr
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Arg Glu Asp Lys Asp Leu His Arg Lys Ile His Arg Ile Ile Gln Gln
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Asp Cys Gln Lys Pro Asn His Met Glu Lys Gly Cys His Phe Leu His
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Ile Leu Ala Cys Ala Arg Leu Ser Ile Arg Pro Gly Leu Ser Glu Ala
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Leu Gln Pro Ala Gly Ser Val Ser Ser Thr Pro Leu Ser Thr Pro Cys
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Ser Ser Val Pro Ser Ser Pro Ser Phe Ser Pro Thr Glu Gln Lys Thr
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His Leu Glu Asp Leu Tyr Trp Met Ala Ser Asn Tyr Gln Gln Met Asn
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Pro Glu Ala Leu Asn Leu Thr Pro Glu Asp Ala Val Glu Ala Leu Ile
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Gly Ser His Pro Val Pro Gln Pro Leu Gln Ser Phe Asp Ser Phe Arg
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Ser Leu Phe Glu Glu Ala His Lys Met Val Arg Glu Ala Asn Met Lys
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Gln Ala Ala Ser Glu Lys Gln Leu Lys Glu Ala Arg Gly Lys Ile Asp
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Thr Pro Ala Ser Pro Asn Arg Glu Leu His Pro Gln Leu Leu Ser Pro
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105

100

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Pro Asp Arg Glu Gly Lys Glu Val Asp Thr Ile Leu Phe Ala Glu Phe
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Gln Ala Trp Arg Glu Ser Pro Thr Leu Asp Lys Thr Cys Pro Phe Leu
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Glu Arg Val Tyr Arg Glu Asp Val Gly Pro Cys Leu Asp Phe Thr Met
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Gln Glu Leu Ser Val Leu Val Arg Ala Ala Val Glu Asp Asn Thr Leu
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Thr Ile Glu Pro Val Ala Ser Gln Thr Leu Pro Thr Val Lys Val Ala
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                                             220
Glu Val Asp Cys Ser Ser Thr Asn Thr Cys Ala Leu Ser Gly Leu Thr
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                                         235
Arg Thr Cys Arg His Arg Ile Arg Leu Gly Asp Ser Lys Ser His Tyr
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                                     250
Tyr Ile Ser Pro Ser Ser Arg Ala Arg Ile Thr Ala Val Cys Asn Phe
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Phe Thr Tyr Ile Arg Tyr Ile Gln Gln Gly Leu Val Arg Gln Asp Ala
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Tyr His Pro Thr Pro Ser Gln Thr Arg Leu Ala Thr Gln Leu Thr Glu
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Glu Glu Gln Ile Arg Ile Ala Gln Arg Ile Gly Leu Ile Gln His Leu
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Ile Ser Gln Gln Leu Gly Leu Glu Leu Asn Thr Val Ser Asn Phe Phe
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Pro Gly Ser Leu Gln Pro Pro Pro Pro Gly Phe Lys Gln Phe Ser Cys
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35
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Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Cys Leu Ser Ser Arg Leu
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Arg Asp Leu Ser Ser Pro Gln Pro Pro Pro Pro Pro Arg Phe Lys Gln Phe
Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp His Arg His Pro Pro Pro
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Arg Pro Ala Asn Phe Cys Ile Phe Ser Arg Asp Glu Val Ser Pro Arg
                           120
Ser Arg Ser Pro Asp Leu Met Xaa Ser Ala His Leu Gly Leu Pro Lys
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                                           140
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Arg Asp Phe Leu Arg Tyr Leu Gln Ser Leu Leu Ala Glu Val Glu Arg
Arg Ile Arg Arg Gly His Ala Arg Leu Ala Leu Ser Gln Asn Gln Gln
Ser Ser Gly Ala Ala Gly Pro Thr Gly Lys Asn Gly Glu Lys Ile Gln
Val Leu Thr Asp Lys Ile Asp Val Leu Leu Gln Gln Ile Glu Glu Leu
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Gly Ser Glu Gly Lys Val Glu Glu Ala Gln Gly Met Met Lys Leu Val
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Glu Gln Leu Lys Glu Glu Arg Glu Leu
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Pro Arg Ala Ser Lys His His Tyr Ser Arg Ser Arg Ser Arg Ser Arg
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Glu Arg Lys Arg Lys Ser Asp Asn Glu Gly Arg Lys His Arg Ser Arg
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Val Asp Glu Ala Gly Ile Asp Gln Asp Gly Val Phe Lys Glu Phe Leu
Glu Glu Ile Ile Lys Arg Val Phe Asp Pro Ala Leu Asn Leu Phe Lys
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Thr Thr Ser Gly Asp Glu Arg Leu Tyr Pro Ser Pro Thr Ser Tyr Ile
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                                    90
His Glu Asn Tyr Leu Gln Leu Phe Glu Phe Val Gly Lys Met Leu Gly
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Lys Ala Val Tyr Glu Gly Ile Val Val Asp Val Pro Phe Ala Ser Phe
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Phe Leu Ser Gln Leu Leu Gly His His His Ser Val Phe Tyr Ser Ser
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Val Asp Glu Leu Pro Ser Leu Asp Ser Glu Phe Tyr Lys Asn Leu Thr
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Ser Ile Lys Arg Tyr Asp Gly Asp Ile Thr Asp Leu Gly Leu Thr Leu
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Ser Tyr Asp Glu Asp Val Met Gly Gln Leu Val Cys His Glu Leu Ile
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Pro Gly Gly Lys Thr Ile Pro Val Thr Asn Glu Asn Lys Ile Ser Tyr
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Ile His Leu Met Ala His Phe Arg Met His Thr Gln Ile Lys Asn Gln
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Gly Gly Phe His Gly Ser His Arg Val Ile Ile Trp Leu Trp Asp Ile
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780

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Leu Lys Glu Tyr Arg Ile Cys Met Pro Leu Thr Val Asp Glu Tyr Lys
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Ile Gly Gln Leu Tyr Met Ile Ser Lys His Ser His Glu Gln Ser Asp
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Arg Gly Glu Gly Val Glu Val Val Gln Asn Glu Pro Phe Glu Asp Pro
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His His Gly Asn Gly Gln Phe Thr Glu Lys Arg Val Tyr Leu Asn Ser
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105

100

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Tyr Asp Met Thr Met Asp Glu Val Arg Glu Phe Glu Arg Ala Thr Gln
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                                                285
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Ser Ser Ile Pro Leu Leu Pro Ser Ser Val Arg Ser Ala Pro Ser Ser
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Arg Gln Leu Xaa Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu
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Asn Cys Pro Glu Asp Leu Ala Gln Leu Glu Glu Leu Ile Asp Met Ala
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7.20	Dha	Tare		T 011	Pro	Dro	Glv	_	Cln	Dro	tro 1	T1a	30 Cvc	T10	Wie
Arg	FIIC	35	ATA	Deu	FIO	FIU	40	Ala	GIII	PIO	vai	45	Cys	116	ura
Sar	A1 =	_	Thr	Trans	Ala	Acn		Len	Sar	17-1	Cvc		Dro	Sar.	Pro
261	50	Cys	1111	пр	AIA	55	ASP	Leu	261	vai	60	ıyı	PIO	Ser	PIO
11:0		m>	T1 -	114 -	Mot		~1··	~1.	ΠЪ~	C		7	G1	C	C
	TIE	IIII	TTE	nis	Met	nis	GLY	GIY	Inr		Ser	ASD	GIY	ser	
65	18 - h	23-	71-	T1.	70	~ 1	<i>~</i> 1	17-1	~1	75	~1	<i>α</i> 1	m\	3	80
Ser	met	Ala	Ala		Tyr	GIY	GIY	vai		GIY	GIY	GIY	Inr	_	ser
a 3	**- 1	•	• • • •	85	a	01		~1	90	~3.	•		~ 3	95	_
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63	.	0	100	3	***	m	7	105	01	m1	.	T	110	*** *	a1
GIA	Leu			ASII	His	rrp		TTE	GIY	Thr	Asp	-	Cys	val	GIU
3	T1.	115.			77 7	3	120	31.	T	3	T	125	01	**- 7	
Arg		ASI	GIU	Mec	Val		Arg	Ata	гÀа	Arg		Ala	GIY	vaı	Asp
D	130	17-3	D	*	3	135	*	~1	•		140		01	a 1	•
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GIN	GIU	Asp	AIA	_	Arg	TTE	Leu	TTE		GIU	Leu	Arg	Asp	_	Pne
D	TT	T	O	165	C		*	T1 -	170	(T)	3		» 1 -	175	0
PIO	. Tyr	Leu		GIU	Ser	lyr	reu	11e	Inr	Inr	Asp	АТА	190	GIY	ser
T1.	33 -	mb	180	TT la sa	D	7	~1		11- 1	**- 7	T	71 -		~ 1	mb
116	AId		MIG	lill	Pro	ASP	_	GIY	vai	vai	Leu		Ser	GIY	Inr
C1	Com	195	C	2	T 011	T10	200	Dwa	7 ~~	C1	C	205	C	~1··	
GIY		ASII	Cys	Arg	Leu		ASII	PIO	ASD	GIY		GIU	ser	GIY	cys
~1	210	T	~1	****	Mot	215	~1	3	~1	~1	220	* 7 -	* ~	C	21-
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225	C 0 TT	N 7 a	T1 174	т	230	77.	wie	~1 ~	71-	235	T	T1.	3703	Dho	240
PFO	ser	AT a	lyr		Ile	Ala	HIS	GIN		val	гåг	ттė	vai		Asp
Co=	т1.	N am	X ===	245	Glu	7 J -	21-	Dwa	250	B ===	T1 a	C1	TT	255	T
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Gla	בומ	Mot		uie	Tyr	Dha	Gln		Dro	Nen.	λνα	Lau		בוד	Tan
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1111	290	Dea	ıyı	Arg	waħ	295	rap	цуз	Cys	Arg	300	MIG	GLY	FIIC	Cys
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T.e.11	Pro	Glu	Tle		Pro	Val	T.e.11	Phe		Glv	Larg	Tle	Glv		Dro
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Tle	Leu				Ser	val				Trn	Glu	T.em			Glu
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Glv	Phe		Leu	Ala	Leu	Thr		Glv	Δτσ	Glu	Tle		Δla	Gln	Δsn
017	370					375	· · · · ·	0 23	3	014	380				
Dhe		Ser	Ser	Phe	Thr		Met	Laze	T.e.11	Ara		Ser	Ser	Δla	T.eu
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	G] v	Ala	Ser	Leu	Gly	Ala	Ara	Hic.	Tle		His	Leu	Leu	Pro	
1	1			405	1		9	****	410	y				415	
Asp	Tvr	Ser	Ala		Ala	Tle	27 =	Dhe		Ser	Tvr	Thr	Phe		
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Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln Glu Val
Met Glu Glu Glu Trp Asn Ala Leu Gln Ser Val Glu Asn Cys Pro Glu
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Glu Ala Ala Trp Val Ser Gln Tyr Lys Asp Ile Thr Asp Val Asp Glu

70

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Cys Ala Ile Leu Asn Ala Val Asn Tyr Ile Ser Thr Val Leu Ala Asp
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Gln Ala Arg Ile Asp Thr Gly Ile His Met Lys Arg Met Gln Thr Pro
Arg His Pro Ala Leu Ser Gln Ser Leu Ile Lys Phe Gly Ile Leu Phe
Asp Pro Ser Ile Phe Phe Leu Glu Thr Gly Ser Arg Phe Ile Ala Gln
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180
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900
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Gln Ile Arg Asp Ile Gln Arg Glu Glu Lys Val Lys Arg Ser Val
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Lys Asp Ala Ala Lys Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala
Lys Glu Met Ile Arg Ser Arg Lys Ala Val Ser Lys Leu Tyr Ala Ser
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Lys Ala His Met Asn Ser Val Leu Met Gly Met Lys Asn Gln Leu Ala
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Val Leu Arg Val Ala Gly Ser Leu Gln Lys Ser Thr Glu Val Met Lys
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Ala Met Gln Ser Leu Val Lys Ile Pro Glu Ile Gln Ala Thr Met Arg
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Glu Leu Ser Lys Glu Met Met Lys Ala Gly Ile Ile Glu Glu Met Leu
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Glu Asp Thr Phe Glu Ser Met Asp Asp Gln Glu Glu Met Glu Glu Glu
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Ala Glu Met Glu Ile Asp Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala
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Leu Gly Lys Ala Pro Ser Lys Val Thr Asp Ala Leu Pro Glu Pro Glu
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Pro Pro Gly Ala Met Ala Ala Ser Glu Asp Glu Glu Glu Glu Glu Glu
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Ala Leu Glu Ala Met Gln Ser Arg Leu Ala Thr Leu Arg Ser
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Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu Glu Arg Met Arg Asn
Ser Arg Asp Arg Leu Leu Asn Arg Tyr Arg Gln Ala Gly Ser Ser Gly
Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln Glu Val Met Glu Glu
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                    70
Glu Trp Asn Ala Leu Gln Xaa Gln Trp Xaa Asn Cys Pro Glu Asp Leu
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90

85

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Ala Gln Leu Glu Glu Leu Ile Asp Met Ala Val Leu Glu Glu Ile Gln
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Gln Glu Leu Ile Asn Gln Glu Gln Ser Ile Ile Ser Glu Tyr Glu Lys
                           120
                                              125
Ser Leu Gln Phe Asp Glu Lys Cys Leu Ser Ile Met Leu Ala Glu Trp
                       135
                                           140
Glu Ala Asn Pro Leu Ile Cys Pro Val Cys Thr Lys Tyr Asn Leu Arg
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                   150
                                       155
Ile Thr Ser Gly Val Val Val Cys Gln Cys Gly Leu Ser Ile Pro Ser
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His Ser Ser Glu Leu Thr Glu Gln Lys Leu Arg Ala Cys Leu Glu Gly
Ser Ile Asn Glu His Ser Ala His Cys Pro His Thr Pro Glu Phe Ser
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                           200
Val Thr Gly Gly Thr Glu Glu Lys Ser Ser Leu Leu Met Ser Cys Leu
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                                          220
Ala Cys Asp Thr Trp Ala Val Ile Leu
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<210> 5967
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660
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840
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1320
ccaaagaagg agetteeett etttattete tttactgetg gattatgtte etteacagee
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Gly Thr Ser Ser Leu Ile Ser Gly Leu Ile Leu Ile Phe Glu Trp Trp
Tyr Phe Arg Lys Tyr Gly Thr Ser Phe Ile Glu Gln Val Ser Val Ser
                        55
His Leu Arg Pro Leu Leu Gly Gly Val Asp Asn Asn Ser Ser Asn Asn
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                                        75
Ser Asn Ser Ser Asn Gly Asp Ser Asp Ser Asn Arg Gln Ser Val Ser
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Glu Cys Lys Val Trp Arg Asn Pro Leu Asn Leu Phe Arg Gly Ala Glu
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Tyr Asn Arg Tyr Thr Trp Val Thr Gly Arg Glu Pro Leu Thr Tyr Tyr
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Asp Met Asn Leu Ser Ala Gln Asp His Gln Thr Phe Phe Thr Cys Asp
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Ser Asp His Leu Arg Pro Ala Asp Ala Ile Met Gln Lys Ala Trp Arg
                                      155
                   150
Glu Arg Asn Pro Gln Ala Arg Ile Ser Ala Ala His Glu Ala Leu Glu
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Ile Asn Glu Thr Arg His Gln Cys Leu Gly Val His Gln Lys Lys Ala
Ser Asn Val Cys Gln Lys Thr Arg Glu Asp Gln Gly Ser Lys Ala Leu
                           200
Leu Glu Leu Gln Ala Tyr Ala Asp Val Gln Ala Val Leu Ala Lys Tyr
                       215
Asp Asp Ile Ser Leu Pro Lys Ser Ala Thr Ile Cys Tyr Thr Ala Ala
                                     235
Leu Leu Lys Ala Arg Ala Val Ser Asp Lys Phe Ser Pro Glu Ala Ala
               245
                                 250
Ser Arg Arg Gly Leu Ser Thr Ala Glu Met Asn Ala Val Glu Ala Ile
           260
                               265
His Arg Ala Val Glu Phe Asn Pro His Val Pro Lys Tyr Leu Leu Glu
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Met Lys Ser Leu Ile Leu Pro Pro Glu His Ile Leu Lys Arg Gly Asp
                      295
                                          300
Ser Glu Ala Ile Ala Tyr Ala Phe Phe His Leu Ala His Trp Lys Arg
                  310
                                      315
Val Glu Gly Ala Leu Asn Leu Leu His Cys Thr Trp Glu Gly Thr Phe
                                  330
               325
Arg Met Ile Pro Tyr Pro Leu Glu Lys Gly His Leu Phe Tyr Pro Tyr
                                                 350
                              345
Pro Ile Cys Thr Glu Thr Ala Asp Arg Glu Leu Leu Pro Ser Phe His
                          360
Glu Val Ser Val Tyr Pro Lys Lys Glu Leu Pro Phe Phe Ile Leu Phe
                       375
Thr Ala Gly Leu Cys Ser Phe Thr Ala Met Leu Ala Leu Leu Thr His
                                       395
                   390
Gln Phe Pro Glu Leu Met Gly Val Phe Ala Lys Ala Val Ser Val Cys
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Leu Glu Gly Gly Leu Gly Glu Trp Met Gly Lys Ala Lys Gly Ile Lys
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<211> 429

<212> DNA

<213> Homo sapiens

<400> 5969

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attgagaaga tootgagoga ggacccccgg tggcaagatg ccaacttcgt gctgggcagc

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Gly Val Leu Ala Ser Gln Ala Met Ile Glu Lys Ile Leu Ser Glu Asp
                            40
Pro Arg Trp Gln Asp Ala Asn Phe Val Leu Gly Ser Tyr Lys Thr Glu
                        55
                                            60
Gln Cys Pro Lys Pro Pro Arg Leu Cys Arg Gln Gly Tyr Ala Cys Pro
                                        75
His Tyr His Asn Ser Arg Asp Arg Arg Asn Pro Arg Arg Phe Gln
                                    90
Tyr Arg Ser Thr Pro Cys Pro Ser Val Lys His Gly Asp Glu Trp Gly
Glu Pro Ser Arg Cys Asp Gly Gly Asp Gly Cys Gln Tyr Cys His Ser
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Arg Thr Glu Gln Gln Phe His Pro Glu Ile Tyr Lys Ser Thr Lys
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300
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420
cccaggactg tggccgtgga tgccagagcg aggatgtgaa tcctgttggg ttctgaagcc
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<210> 5972
<211> 104
<212> PRT
<213> Homo sapiens
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Cys Pro Asn Arg Gln His Pro Tyr Phe Ile Asp Gly His Pro His Phe
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Arg Asp Ser Ser Leu Leu Tyr Pro His Phe Thr Gly Glu Gly Ile Glu
Ala Gln Lys Val Arg Ser Leu Leu Gln Asp Asp Gln Leu Asn Gln Asn
Phe Arg Ala Ser Asn Thr Lys Cys Val Pro Leu Ser Ser Val Ser His
Leu Leu Pro Arg Gly Ser Ala Ser Ser Leu Trp Pro Leu Ser Ile Leu
Pro Pro Thr Leu Leu Pro Ala Ser
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240
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480
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Pro His Pro Gly Leu Ser Pro Thr Ser Gly Thr Leu Met Pro Gly Arg
                        55
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Arg Arg Gly Gly Pro Ser Phe Gly Thr Pro Ala Leu Arg Arg Arg Lys
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Cys His Arg Glu Ala Pro Ala Ser Gly Leu Ser Thr Ala Ala Arg Glu
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420
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325
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Ala Asn Ile Leu Leu Tyr Ile Gln Arg Thr Lys Ser Met Phe Gln Arg
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Thr Thr Tyr Lys Tyr Glu Met Ile Asn Lys Gln Asn Glu Gln Met His
        355
                            360
                                                 365
Ala Leu Leu Ala Ile Ala Leu Thr Met Tyr Pro Met Arg Ile Asp Glu
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Met Gln Lys Gly Asp Pro Gln Val Tyr Glu Glu Leu Phe Ser Tyr Ser
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Cys Pro Lys Phe Leu Ser Pro Val Val Pro Asn Tyr Asp Asn Val His
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Leu Thr Glu Gln Glu Phe Arg Ile Gln Leu Leu Val Phe Lys His Lys
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Tyr Met Gln Gly Leu Ser Ala Cys Glu Gln Ile Arg Ala Ala Leu Tyr
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Lys Phe Ala Asn Asp Glu Asn Val Lys His Ile Ser Cys Pro Leu Leu
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Lys Leu Tyr Ser Ile Ala Ala Pro Ala Arg Ser Phe Arg Asp Phe Lys
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Val Gln Phe Val Pro Phe His Ser Asp Leu Gly Tyr Arg His Lys Tyr
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Leu Lys Gly Glu Lys Gly Glu Ser Ala Ser Gln Pro Thr Gly Glu Pro
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Gly Ser Ala His Ser Glu Pro Gly Pro Pro Gly Pro Pro Pro Pro
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Pro Gly Pro Val Gly Pro Pro Gly Leu Ile Gly Leu Pro Gly Thr Lys
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Gly Glu Lys Gly Arg Pro Gly Glu Pro Gly Leu Asp Gly Phe Pro Gly
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Arg Gly Val Pro Gly Arg Lys Gly Val Lys Gly Gln Lys Gly Glu Pro
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Ser Ser Thr Asn Thr Val Gly Ala Thr Val Asn Ser Gln Ala Ala Gln
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Ala Gln Pro Pro Ala Met Thr Ser Ser Arg Lys Gly Thr Phe Thr Asp
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Met Ala Arg Lys Phe Ser Ala Pro Gly Gln Leu Cys Ile Ser Met Thr
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Ser Asn Leu Gly Gly Ser Ala Pro Ile Ser Ala Ala Ser Ala Thr Ser
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Pro Ala Thr Pro Phe Gly Ala Gln Trp Ser Gly Thr Gly Gly Pro Ala
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Glu Thr Tyr Ser Asn Arg Val Ser Ser Ile Ser Pro Gly Ser Ala Thr
Leu Leu Ser Ser Phe Gly Ala Trp Asp His Ile Cys Asn Met Arg Tyr
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Ile Met Phe Asp Lys Asp Asn Leu Asp Asp Met Gly Tyr Ile Val Glu
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Asn Asp Val Ile Met His Ala Leu Thr Lys Gln Leu Glu Ala Val Ser
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Asp Arg Val Thr Val Leu Tyr Arg Ser Lys Ala Ile Arg Tyr Thr Trp
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Pro Cys Pro Phe Pro Met Ala Asp Ser Ser Pro Trp Val His Ile Thr
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Leu Gly Asp Gly Ser Thr Phe Gln Thr Lys Leu Leu Ile Gly Ala Asp
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Trp Asn Tyr Asp Gln Ser Ala Val Val Ala Thr Leu His Leu Ser Glu
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Ala Thr Glu Asn Asn Val Ala Trp Gln Arg Phe Leu Pro Ser Gly Pro
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Glu His Leu Lys His Gln Thr Val Tyr Arg Leu Leu Lys Cys Ala Pro
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Arg Gly Lys Asn Gly Phe Thr Pro Leu His Met Ala Val Asp Lys Asp
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Thr Thr Asn Val Gly Arg Tyr Pro Val Gly Arg Phe Pro Ser Leu His
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Ala Ile Met Asn Ala Leu Ile Glu Ala Gly Ala His Met Asp Ala Thr
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105

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Leu Val Ile Leu Gly Cys Ile Arg Ala Gly Leu Ile Phe Met Pro Gly
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Arg Asp Leu Gln Glu Ile Cys Arg Lys Gln Gly Val Ala Val Tyr Ile
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Leu Leu Asp Gln Ala Leu Leu Ser Gln Phe Leu Asp Met Cys Met Asp
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75
Leu Lys Val His Pro Glu Gln Glu Lys Leu Met Thr Val Arg Thr Ile
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Thr Gly Asn Ile Tyr Tyr Ala Arg Ser Gly Thr Lys Ile Ile Gly Lys
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Val His Glu Lys Phe Thr Leu Ile Asp Gly Ile Arg Val Ala Thr Gly
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Ser Tyr Ser Phe Thr Trp Thr Asp Gly Lys Leu Asn Ser Ser Asn Leu
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Val Ile Leu Ser Gly Gln Val Val Glu His Phe Asp Leu Glu Phe Arg
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Ile Leu Tyr Ala Gln Ser Lys Pro Ile Ser Pro Lys Leu Leu Ser His
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Phe Gln Ser Ser Asn Lys Phe Asp His Leu Thr Asn Arg Lys Pro Gln
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Ser Lys Glu Leu Thr Leu Gly Asn Leu Leu Arg Met Arg Leu Ala Arg
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Leu Ser Ser Thr Pro Arg Lys Ala Asp Leu Asp Pro Glu Met Pro Ala
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Glu Gly Lys Ala Glu Arg Lys Pro His Asp Cys Glu Ser Ser Thr Val
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Lys Ala Ile Asp Ala Ala Thr Gln Thr Glu Pro Gly Glu Glu Met Pro
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Cys Ala Gly Thr Gln Thr Ala Val Ile Thr Arg Ile Ala Ser Ser Gln
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Thr Thr Ile Trp Ser Arg Ser Thr Thr Thr Gln Thr Asp Met Asp Glu
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Asn Ile Leu Phe Pro Arg Gly Thr Gln Ser Thr Glu Gly Ser Pro Val
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Ser Lys Met Ser Val Ser Arg Ser Ser Ser Leu Lys Ser Ser Ser Ser
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Val Ser Ser Gln Gly Ser Val Ala Ser Ser Thr Gly Ser Pro Ala Ser
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Ile Arg Thr Thr Asp Phe His Asn Pro Gly Tyr Pro Lys Tyr Leu Gly
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Thr Pro His Leu Glu Leu Tyr Leu Ser Asp Ser Leu Arg Asn Leu Asn
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                                395 400
Lys Glu Arg Gln Phe His Phe Ala Gly Ile Arg Ser Arg Leu Asn His
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                            410 415
Met Leu Ala Met Leu Ser Arg Arg Thr Leu Phe Thr Glu Asn His Leu
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His Leu Pro Ser Ala Cys Leu Gly Ala Arg Arg Ser Ser Leu Leu
Gly Tyr Gly Ser Cys Arg Asp Thr Gln Ser Trp Thr Pro Asp Pro Leu
Pro His Pro Pro Ser Leu Ser Pro Gln Ser Leu Leu Tyr Ser Gln Ala
               85
Met Arg Ser Pro Ile Ser His Gln Glu Leu Thr Arg Pro Leu Gly Lys
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Glu Ala Ala Arg Arg Arg Cys Gly His Thr Val Ala Leu Ser Ala Arg
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Ala Lys Lys Arg Lys Leu Asn Ser Ser Ser Ser Ser Ser Asn Ser
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Ser Asn Glu Arg Glu Asp Phe Asp Ser Thr Ser Ser Ser Ser Thr
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Pro Pro Leu Gln Pro Arg Asp Ser Ala Ser Pro Ser Thr Ser Ser Phe
Cys Leu Gly Val Ser Val Ala Ala Ser Ser His Val Pro Ile Gln Lys
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Lys Leu Arg Phe Glu Asp Thr Leu Glu Phe Val Gly Phe Asp Ala Lys
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Met Ala Glu Glu Ser Ser Ser Ser Ser Ser Ser Ser Pro Thr Ala
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Thr Gly His Glu Leu Leu Ser Glu Leu Gln Gln Arg Arg Phe Asn Gly
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Ser Asp Gly Gly Val Ser Trp Ser Pro Met Asp Asp Glu Leu Leu Ala
Gln Pro Gln Val Met Lys Leu Leu Asp Ser Leu Arg Glu Gln Tyr Thr
Arg Tyr Gln Glu Val Cys Arg Gln Arg Ser Lys Arg Thr Gln Leu Glu
Glu Ile Gln Gln Lys Val Met Gln Val Val Asn Trp Leu Glu Gly Pro
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Gly Ser Glu Gln Leu Arg Ala Gln Trp Gly Ile Gly Asp Ser Ile Arg
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Ala Ser Gln Ala Leu Gln Gln Lys His Glu Glu Ile Glu Ser Gln His
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Gln Gln Gln Leu Ser Asp Val Cys Tyr Arg Gln Ala Ser Gln Leu Glu
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Asp Val Ala Pro Ala Asp Gly Ala Ser Ile Gln Gln Thr Leu Lys Leu
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Leu Glu Glu Lys Leu Lys Ser Val Asp Val Gly Leu Gln Gly Leu Arg
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Gly Pro Met Glu Arg Met Xaa Thr Ile Glu Asn Lys Glu Asn Val Asp
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His Ile Gln Gly Val Met Glu Asp Met Gln Leu Arg Lys Gln Arg Cys
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Glu Asp Met Val Asp Val Arg Arg Leu Lys Met Leu Gln Met Val Gln
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Leu Phe Lys Cys Glu Glu Asp Ala Ala Lys Ala Val Glu Trp Leu Ser
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Glu Leu Leu Asp Ala Leu Leu Lys Thr His Ile Arg Leu Gly Asp Asp
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Ala Gln Glu Thr Lys Val Leu Leu Glu Lys His Arg Lys Phe Val Asp
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Val Ala Gln Ser Thr Tyr Asp Tyr Gly Àrg Gln Leu Leu Gln Ala Thr
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Val Val Leu Cys Gln Ser Leu Arg Cys Thr Ser Arg Ser Ser Gly Asp
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Thr Leu Pro Arg Leu Asn Arg Val Trp Lys Gln Phe Thr Ile Ala Ser
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Thr Ala His Tyr Asp Pro Gly His Cys Phe Ala Glu Ser Arg Glu Leu
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Gly Arg Gly Ala Ala Val Cys Ala Tyr Val Arg Met Val Phe Leu Ala
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Leu Tyr Val Leu Phe Leu Ala Asp Glu Glu Phe Asp Val Val Cys
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Asp Gln Val Ser Ala Cys Ile Pro Val Phe Arg Leu Ala Arg Arg Arg
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Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp Leu Leu Leu Thr Lys
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Ile Ile Glu Asp Trp Asp Leu Met Glu Arg Phe Met Glu Gln Val Val
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 Pro Gly Leu Pro Phe Gly Gln Gly Ala Val Ala Arg Ala Ala Pro Cys
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His Arg Tyr His Arg Lys Glu Asn Leu Glu Tyr Cys Ile Met Val Ile
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Gln His Leu Arg Lys Gly Lys Ala Thr Arg Val Gly Glu Pro Gly
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Ile Thr Arg Ala Val Met Ser Lys Ile Gln Val Glu Ser Ser Gly Ala
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Arg Pro Ser Thr Leu Ser Arg Ala Leu Gln Ala Ser Gly Thr Cys Arg
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T 0.11	C1	T1.	180	77.	T	7~~	חות	185	Glu.	Thr	Val.	Val		Dro	Glu
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Pro Leu Ala Leu Gln Leu Glu Gln Leu Leu Asn Pro Arg Pro Ser Glu
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Gly Ser Ile Arg Lys Leu Ala Ser Ala Ser Leu Leu Asp Thr Asp Lys
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Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
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Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
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Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val
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Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro
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Leu Ile Val Glu Gly His Leu Thr Lys Ala Val Glu Glu Thr Lys Leu
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Ser Lys Glu Asn Gln Thr Arg Ala Lys Glu Ser Asp Phe Ser Asp Thr
Leu Ser Pro Ser Lys Glu Lys Ser Ser Asp Asp Thr Thr Asp Ala Gln
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Val Cys Val Cys Val Ser Val Cys Val Cys Val His Thr Gly
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	Ser	Thr	Tyr	Lys		Ser	Asn	Thr	Leu		Leu	Pro	Thr	Glu	
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- •	690	_	_		_,	695	-1		_		700			-1 -	Db -
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910

905

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Leu Pro Pro Thr Glu Phe Ala Gln Leu Ile Lys Arga Gln Gln Gln
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                                           940
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                                       955
Phe Arg His Met Asn Gln Gly Asp Ala Gly Ser Leu Ala Pro Ser Leu
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Gly Gln Ser Met Thr Glu Arg Gln Ala Leu Ser Tyr Gln Asn Ala
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Asp Ser Tyr His His Thr Ile Gln Asn Ser Asp Asp Ala Tyr Val Gln
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Leu Asp Asn Leu Pro Gly Met Ser Leu Val Ala Gly Lys Ala Leu Ser
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Arg	Arq	Arq	Thr	Ser	Ser	Lvs	Ser	Glu	Ala	Glv	Ala	Arq	Glv	Glv	
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C1.,	210	C1	C1	~1	Th.	215	The	77-7	N	T	220	C	C	Dh-	D
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	Ser	I.e.i	Thr	λla		Ara	Gly	Dro	710		בומ	Pro	Gln	Val	
ALG	JCI	Deu	****	245	Der	Arg	Gry	FIU	250	AIG	ALG	FIO	GIII	255	FIO
Leu	Asp	Glv	Ala		Thr	Ser	Val	Phe		Asn	Δςη	Val	Val		Va 1
		1	260	<u>-</u>				265					270		
Thr	Glv	Asn	Tyr	Val	Leu	Asp	Arg		Asp	Leu	Val	Glu		Gln	Thr
	•	275					280					285			
Pro	Glu	Tyr	Asp	Val	Val	Leu	Cys	Leu	Ser	Leu	Thr	Lys	Trp	Val	His
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Leu	Asn	Trp	Gly	Asp	Glu	Gly	Leu	Lys	Arg	Met	Phe	Arg	Arg	Ile	Tyr
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Arg	His	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Val	Leu	Glu	Pro	${\tt Gln}$	Pro	Trp
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Ser	Ser	Tyr	Gly	Lys	Arg	Lys	Thr	Leu	Thr	Glu	Thr	Ile	Tyr	Lys	Asn
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Tyr	Tyr	Arg	Ile	Gln	Leu	Lys	Pro	Glu	Gln	Phe	Ser	Ser	Tyr	Leu	Thr
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Ser		Asp	Val	Gly	Phe		Ser	Tyr	Glu	Leu		Ala	Thr	Pro	His
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	Thr	Ser	Lys	Gly		Gln	Arg	Pro	Val	_	Leu	Phe	His	Lys	
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Arg	ser	Pro	Ser												
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Pro Ala Cys Leu Leu Gly Arg Pro Trp Met Ser Arg Arg Cys Ser Arg
        35
                            40
Leu Gly Ser Thr Pro Pro Pro Ala Pro Ala Ser Pro Val Glu Ser Pro
                        55
                                            60
Arg Pro Ser Pro Ala Ser Ser Ala Phe Ser Ser Leu Pro Ser Asp Gly
                                                             80
                    70
                                        75
Trp Gly Ser Ser Val Gly Ser Gly Leu Pro Trp Pro Ala Thr Arg Trp
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Ser Thr Cys Pro Arg Trp Arg Thr Asp Val Ser Pro Ala Asp Thr Ile
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Ala Pro Arg Ser Trp Leu Leu Pro Leu Ser Ala Thr
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1260
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Pro Gly Ala Ala Ala Gly Leu Thr Leu Leu Cys Ser Leu Val Pro Ile
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Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser Arg
Gln Lys Ala Leu Ser Leu Val Ser Cys Phe Ala Gly Gly Val Phe Leu
Ala Thr Cys Leu Leu Asp Leu Leu Pro Asp Tyr Leu Ala Ala Ile Asp
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Glu Ala Leu Ala Ala Leu His Val Thr Leu Gln Phe Pro Leu Gln Glu
                               105
Phe Ile Leu Ala Met Gly Phe Phe Leu Val Leu Val Met Glu Gln Ile
                           120
Thr Leu Ala Tyr Lys Glu Gln Ser Gly Pro Ser Pro Leu Glu Glu Thr
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                       135
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Gly Pro Gly Val Pro Gln Ala Ser Gly Ala Pro Ala Thr Pro Ser Ala
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Leu Arg Ala Cys Val Leu Val Phe Ser Leu Ala Leu His Ser Val Phe
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                           200
                                              205
Leu Cys Leu Ala Leu Leu His Lys Gly Ile Leu Ala Val Ser Leu
    210
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Cys Gly Ile Leu Phe Ser Cys Met Thr Pro Leu Gly Ile Gly Leu Gly
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Val Leu Glu Gly Met Ala Ala Gly Thr Phe Leu Tyr Ile Thr Phe Leu
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                           280
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Glu Ile Leu Pro Gln Glu Leu Ala Ser Ser Glu Gln Arg Ile Leu Lys
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720

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Val Ala Gln Ala Gly Val Xaa Trp His Ser Leu Gly Ser Leu Gln Pro
                                25
Pro Leu Pro Gly Phe Lys Gln Phe Ser Cys Arg Ser Leu Pro Ser Ser
                            40
Trp Asp Tyr Arg His Ala Pro Pro Arg Gln Ala Asn Phe Cys Ile Phe
Ser Arg Asp Gly Val Ser Pro Cys Trp Pro Gly Trp Ser Gln Thr Pro
Asp Leu Arg Arg Ser Thr His Leu Ser Val Pro Lys Cys Trp Asp Tyr
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Arg Arg Glu Pro Pro His Leu Ala Tyr Glu Trp Ser Phe Asn
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Pro Gly Val Pro Asn Ser Ala Pro Phe Lys Glu Ala Leu Leu Glu Glu
Ala Glu Leu Arg Lys Gln Arg Leu Glu Glu Leu Lys Gln Gln Gln Lys
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Gln Val Lys Thr Pro Thr Leu Gln Val Arg Gly Ala Ser Ala Leu Ala
Pro Gln Phe Pro Gln Arg Asn Arg Leu Leu Ala Ser Arg Val Gly Tyr
Arg Val Ser Val Leu His Gly Ile Tyr Glu Asp Val Pro Pro Lys Leu
                    70
Leu Pro Pro Pro Pro Trp Asp Ala Thr Val Arg Pro Ala Asp Glu Phe
                                    90
Leu Pro Gln Arg Pro Arg Glu Gly Gly Leu Arg Ala Ala Ala Ala Ala
                                105
Thr Gly Gly Glu Ala Ser Ala Gly Asn Leu Gly Pro Gly Gly Ala Arg
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Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
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Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
                        55
    50
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
                                        75
                    70
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
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Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
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Gln Arg Gly Pro Thr Glu Leu Met Pro Ala Cys Phe Lys Pro Thr Asn
Glu Asn Ser Pro Trp Glu Thr Cys Leu Asp Asn Thr Leu Asp Pro Asn
Lys Cys Phe Asn Pro Thr Ser Pro Leu Ser Leu Pro Leu Ser Cys Pro
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Tyr Pro Leu Val Glu His Val Cys Pro Lys Arg Pro Cys Lys Val Cys
                                    90
Cys Pro Val Leu Ser Gly Leu Cys Gln Gly Ile Lys Leu Leu Leu
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Cys Asp Val Ser Cys Cys
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Cys His Ile Cys Phe Glu Leu Asn Ile Glu Gly Val Pro Lys Ser Asp
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Leu Leu His Thr Lys Ser Leu Arg Gly His Lys Asp Cys Phe Glu Lys
Tyr His Leu Ile Ala Asn Gln Gly Cys Pro Arg Ser Lys Leu Ser Lys
                                        75
65
Ser Thr Tyr Glu Glu Val Lys Thr Ile Leu Ser Lys Lys Ile Asn Trp
                                    90
Ile Val Gln Tyr Ala Gln Asn Lys Asp Leu Asp Ser Asp Ser Glu Cys
            100
                                105
                                                    110
Ser Lys Lys Pro Gln His His Leu Phe Asn Phe Arg His Lys Pro Glu
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                            120
Glu Lys Leu Leu Pro Gln Phe Glu Ser Gln Val Pro Lys Tyr Ser Ala
                        135
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Arg Gly Leu Val Pro Thr Asp Tyr Val Glu Ile Leu Pro Ser Asp Gly
Lys Asp Gln Phe Ser Cys Gly Asn Ser Val Ala Asp Gln Ala Phe Leu
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Asp Ser Leu Ser Ala Ser Thr Ala Gln Ala Ser Ser Ser Ala Ala Ser
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Ala Ser Lys Ser Gly Asn Trp Glu Ser Ser Glu Gly Trp Gly Ala Gln
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GIII	Leu	275	F10	1111	nom	****	280	•••		• • • •		285		2	-1-
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Dro		בומ	Pro	Δsn	Leu		Leu	Val	Glu	Ile		Gln	Lvs	Cvs	Glu
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				485					490					495	Tyr
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Leu Leu Ser Leu Glu His Val Gly Ile Leu His Lys Asp Phe Glu Ser
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Ile Leu Pro Thr Arg Lys Asn His Asn Met Ala Ser Arg Pro Leu Thr
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Leu Cys Lys Thr Glu Asn Lys Ala Lys Ser Gly Lys Gln Asn Ser Lys
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Gln Val Glu Glu Ala Ile Val Gln Ser Gly Gln Lys Lys Leu Val Leu
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Leu Asn Tyr Leu Lys Lys Glu Leu Pro Thr Val Val Phe Arg Ala Ser
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Ile Asp Ser Pro Ser Phe Ile Val Ser Pro Leu Asn Ser Ser Ser Ala
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Lys Gln Glu Glu Arg Glu Asp Asp Lys Asp Ser Asp Gln Glu Thr Val
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215

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Gly Ala Asn Gly Glu Gln Lys Asp Ser Asp Thr Glu Lys Gln Gly Pro
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Glu Arg Lys Arg Ile Lys Lys Glu Pro Val Thr Arg Lys Ala Gly Leu
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Leu Phe Gly Met Gly Leu Ser Gly Ile Arg Ala Gly Tyr Pro Leu Ser
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Glu Arg Gln Gln Val Ala Leu Leu Met Gln Met Thr Ala Glu Glu Ser
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Val Cys Gln Lys Gly Thr Pro Asn Ser Ala Ser Lys Thr Lys Asp Lys
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Leu Asn Lys Arg Asn Glu Arg Gly Glu Thr Arg Leu His Arg Ala Ala
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Ile Arg Gly Asp Ala Arg Arg Ile Lys Glu Leu Ile Ser Glu Gly Ala
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Asp Val Asn Val Lys Asp Phe Ala Gly Trp Thr Ala Leu His Glu Ala
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Ala Ala Asn Asn Gly His Tyr Lys Val Val Lys Leu Leu Leu Arg Tyr
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Val Ala Asn Ser Pro Thr Met Val Asn Leu Leu Leu Gly Lys Gly Thr
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Tyr Thr Ser Ser Glu Glu Ser Ser Thr Glu Ser Ser Glu Glu Glu Asp
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Gln Lys Ala Thr Ala Pro Val Lys Asp Glu Tyr Glu Phe Asp Glu Asp
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Lys Asp Tyr Arg Lys Glu Thr Lys Ser Asn Ser Phe Ile Ser Ile Pro
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Lys Met Glu Val Lys Ser Tyr Thr Lys Asn Asn Thr Ile Ala Pro Lys
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Lys Ala Ser His Arg Ile Leu Ser Asp Thr Ser Asp Glu Glu Asp Ala
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Leu His Pro Leu Gly Ala Ala Ser Ala Gly Arg Ala Leu Glu Pro Lys
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Ala Asp Pro His Thr Cys Pro Tyr Gly Arg Lys Glu Ser Arg Gly Glu
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Glu Met Leu Ser Lys Lys Gln Glu Phe Leu Glu Lys Lys Ile Glu Gln
Glu Leu Thr Ala Ala Lys Lys His Gly Thr Lys Asn Lys Arg Ala Ala
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Ser Thr Ala Ile Ser Lys Pro Val Gly Phe Gly Glu Glu Phe Asp Glu
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Asp Glu Leu Met Ala Glu Leu Glu Glu Leu Glu Glu Glu Glu Leu Asp
                               185
Lys Asn Leu Leu Glu Ile Ser Gly Pro Glu Thr Val Pro Leu Pro Asn
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Tyr Leu Phe Ser Leu Pro Ile Lys Glu Ser Glu Ile Ile Asp Phe Phe
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Leu Gly Ala Ser Leu Lys Asp Glu Val Leu Lys Ile Met Pro Val Gln
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His Thr Val Pro Cys Lys Val Thr Gly Arg Cys Gly Ser Val Leu Val
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Pro Lys Lys Leu Leu Met Met Ala Gly Ile Asp Asp Cys Tyr Thr Ser
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Arg Lys Met Gly Leu Arg Pro Gly Val Arg His Pro Leu Leu Gly Asp
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Tyr Arg Arg Val Pro Asn Ser Asn Pro Pro Glu Tyr Glu Phe Leu Trp
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90

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 Val Val Asp Glu Ala Ile Asp Ser Leu Ala Arg Thr Lys Gly Val Met
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 Lys Pro Pro Cys Ser Glu Gly Ser Pro Trp Arg Cys Pro His Phe Thr
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Gln Glu Asp Pro Glu Asp Leu Asp Gly Ser Val Gln Gly Val Lys Pro
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Gln Lys Ala Ala Ser Ser Thr Ser Ser Gly Ser His His Ser Ser His
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240
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Ala Gln Leu Ser His Cys Lys Ser Leu Gly His Phe Glu Asn Leu Gln
Lys Tyr Lys Ala Ala Lys Asn Pro Ser Pro Thr Thr Arg Pro Val Ser
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Arg Arg Cys Ala Ile Asn Ala Arg Asn Ala Leu Thr Ala Leu Phe Thr
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Ser Ser Gly Arg Pro Pro Ser Gln Pro Asn Thr Gln Asp Lys Thr Pro
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Ser Lys Val Thr Ala Arg Pro Ser Gln Pro Pro Leu Pro Arg Arg Ser
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Gly Gly Pro Ala Pro Ser Pro Gln Xaa Tyr Ile His Asp Ser Pro Ser
Cys Trp Pro Trp Thr Lys Ala Gly Ser Ser Xaa Cys Pro Val Arg Ser
Pro Tyr Ser Pro Pro Ala Ala Arg Pro Gly Pro Gly Xaa Pro Leu Trp
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Cys Gln Arg Val Ser Gln Asn Pro Gly Pro Ser Pro Ser Xaa Gly Pro
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Leu Pro Ser Pro Arg Pro Val Cys Trp Asp Gly Ala Ser Thr Leu Arg
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Leu Ile Gln Asp Gln Asn Ala Gln Thr Arg Trp Lys Gln Gly Arg Tyr
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Pro Tyr Arg Cys His Asp Cys Gly Lys Cys Phe Arg Gln Leu Ala Tyr
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Leu Val Glu His Lys Arg Ile His Thr Lys Glu Lys Pro Tyr Lys Cys
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Ser Lys Cys Glu Lys Thr Phe Ser Gln Asn Ser Thr Leu Ile Arg His
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Gln Val Ile His Ser Gly Glu Lys Arg His Lys Cys Leu Glu Cys Gly
Lys Ala Phe Gly Arg His Ser Thr Leu Leu Cys His Gln Gln Ile His
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Ser Lys Pro Asn Thr His Lys Cys Ser Glu Cys Gly Gln Ser Phe Gly
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Leu Phe Arg His Gln Val Ile His Thr Gly Ser Gln Leu Tyr Gln Cys
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Asn Pro Glu Gly Gly Val Asn His Glu Asn Gly Met Asn Arg Asp Gly
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Gly Met Ile Pro Glu Gly Gly Gly Asn Gln Glu Pro Arg Gln Gln
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Pro Gln Pro Pro Pro Glu Glu Pro Ala Gln Ala Ala Met Glu Gly Pro
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Leu Gln Val Glu Glu Leu Glu Ser Val Phe Arg His Thr Gln Tyr Pro
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Val Gly Gln Trp Thr Gly Thr Glu Leu His Phe Thr Ala Leu Ile Asn
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Cys Met Glu Gly Ile Cys Lys Pro Asp Pro Arg Ile Tyr Lys Leu Cys
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Leu Gly Thr Asn Leu Lys Glu Ala Ala Arg Leu Gly Ile His Thr Ile
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Lys Val Asn Asp Pro Glu Thr Ala Val Lys Glu Leu Glu Ala Leu Leu
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Gly Phe Thr Leu Arg Val Gly Val Pro Asn Thr Arg Pro Val Lys Lys
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Thr Met Glu Ile Pro Lys Asp Ser Leu Gln Lys Tyr Leu Lys Asp Leu
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Val Gly Thr Glu Lys Gly Arg Met Phe Leu Asn Ala Arg Lys Glu Leu
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Glu Ala Glu His Pro Lys Lys Val Gln Arg Gly Glu Gly Gly Arg
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T	///	7 ~~	Ala	325	т1.	Tura	G111	Thy	330	7 cn	Tla	Aen	Thr		Δτα
Lys	irp	Asp	340	Pne	TIE	гуз	Giu	345	Giu	ASP	116	ASII	350	шси	y
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His	Ser	Ile	His	Phe	Ile	Ile	Lys		Met	Phe	Asp	Glu		Ile	Phe
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Thr	Gly		Lys	Pne	Thr	гÀг		Thr	Thr	гÀг	ren	445	PIO	Ald	Ser
D	D	435	Asp	The second	Co~	. ד ג	440	Wa 1	Ca*	7~~	בות		17a 1	1.411	Δen
Pro	450		Asp	1111	261	455	GIU	val	261	Arg	460	1111	Val	Deu	nsp
T.e.11			Asn	Ala	Ara		Asp	Lvs	Glv	Ser		Ser	Glu	Asp	Cvs
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val	тте	Arg	Pro		Arg	гÃг	GIN	val	570	ren	neu	Fue	Mail	575	AL G
The same	בו מ	Lare	א ו ~	565	G111	T1 c	Sar	Gl ss		1/= 1	Lve	Val	Pro		Ser
1 A L	ALG	nys	580	116	Gry	116	261	585	-10	vai	2,3	A 400 mg	590		
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Thr	Ser	Ala	Phe	Ser	Arg	Ala	Thr	Arg	Asp	Pro	Phe	Ala	Pro	Ser	Arg
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でトー		T/a T	Dro	7 1 a	Th~		Th~	The	Ce~	Gly		Trn	Gl 11	ጥኮ~	G1n
625	-10	V 44 ±	210	ALA	630	110		****		635			 u		640
023					0.50										
G7 11	6111	Den	Tare	Acr	ጥኮ፦	2] =	ייוני	Den	Ser	Ser	Thr	Δla	Acn	Arm	ייידע
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Cys	Ser	Cys 995	Ile	His	Phe	Thr	Asn 1000		Ser	Ile	Leu	Ile 1005		Thr	Asn
Lys	Phe	Tyr	Glu	Ile	Asp	Met	Lys		Tyr	Thr	Leu			Phe	Leu

1015

1020

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Asp Lys Asn Asp His Ser Leu Ala Pro Ala Val Phe Ala Ala Ser Ser
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Asn Ser Phe Pro Val Ser Ile Val Gln Val Asn Ser Ala Gly Gln Arg
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Glu Glu Tyr Leu Leu Cys Phe His Glu Phe Gly Val Phe Val Asp Ser
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Tyr Gly Arg Arg Ser Arg Thr Asp Asp Leu Lys Trp Ser Arg Leu Pro
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Leu Ala Phe Ala Tyr Arg Glu Pro Tyr Leu Phe Val Thr His Phe Asn
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Ser Leu Glu Val Ile Glu Ile Gln Ala Arg Ser Ser Ala Gly Thr Pro
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Ala Arg Ala Tyr Leu Asp Ile Pro Asn Pro Arg Tyr Leu Gly Pro Ala
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Ile Ser Ser Gly Ala Ile Tyr Leu Ala Ser Ser Tyr Gln Asp Lys Leu
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                           1145
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Arg Val Ile Cys Cys Lys Gly Asn Leu Val Lys Glu Ser Gly Thr Glu
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His His Arg Gly Pro Ser Thr Ser Arg Ser Ser Pro Asn Lys Arg Gly
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Pro Pro Thr Tyr Asn Glu His Ile Thr Lys Arg Val Ala Ser Ser Pro
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Arg Tyr Arg Glu Gly Arg Thr Glu Leu Arg Arg Asp Lys Ser Pro Gly
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                                             1230
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Arg Glu Thr Ala Gly Ser Arg Pro Ala Ala Arg Ser Pro Gly Arg Glu
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Ile Leu Phe Ile Cys Ala Arg Gly Arg Arg Gly Asn Pro Cys Leu Ser
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Leu Ser Gln Arg Arg Val Glu Ala Ala His Val Leu Gly His Arg Glu
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                                    90
Trp Ser Glu Lys Arg Gln Lys Lys Asp Ile Pro Trp Ser Trp Arg Gln
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Val Ile Ala Thr Asp Ile Asn Glu Ser Lys Leu Gln Glu Leu Glu Lys
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Tyr Pro Gly Ile Gln Thr Arg Val Leu Asp Val Thr Lys Lys Lys Gln
 Ile Asp Gln Phe Ala Asn Glu Val Glu Arg Leu Asp Val Leu Phe Asn
                                         75
                     70
 Val Ala Gly Phe Val His His Gly Thr Val Leu Asp Cys Glu Glu Lys
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 Asp Trp Asp Phe Ser Met Asn Leu Asn Val Arg Ser Met Tyr Leu Met
                                 105
 Ile Lys Ala Phe Leu Pro Lys Met Leu Ala Gln Lys Ser Gly Asn Ile
                                                 125
                             120
         115
 Ile Asn Met Ser Ser Val Ala Ser Ser Val Lys Gly Val Val Asn Arg
                         135
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 Cys Val Tyr Ser Thr Thr Lys Ala Ala Val Ile Gly Leu Thr Lys Ser
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                     150
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165 170 175 Pro Gly Thr Val Asp Thr Pro Ser Leu Gln Glu Arg Ile Gln Ala Arg 185 Gly Asn Pro Glu Glu Ala Arg Asn Asp Phe Leu Lys Arg Gln Lys Thr 200 Gly Arg Phe Ala Thr Ala Glu Glu Ile Ala Met Leu Cys Val Tyr Leu 215 Ala Ser Asp Glu Ser Ala Tyr Val Thr Gly Asn Pro Val Ile Ile Asp 230 235 Gly Gly Trp Ser Leu 245 <210> 6251 <211> 1611 <212> DNA <213> Homo sapiens <400> 6251 tattgctgac atgcaggaag agtccccatg tagtacaaaa atatgtcttt atacaaactt ttttgtgact ttttccgttt ctttacaata ggacttctct cagtgtgtga cacccagtga gggctgaccc atcctcctct cctttgcttc accaggaatg tcatcagaca catggcttga 240 cettggaagg geceagtetg tetgacaggg etttgeagae eeggeggeta ttgetttgaa aaggaggaga aagaccacgc acgggcagca gcctggaggg acccggtggg ctgctgagag ggggctccgc tgcgacgggc cctggcccag cttcaggccc tcacaggagg acagtcaagg 420 gctgggagcc ctaggccgga ctgcatttcc gctcccgcag gagactttct atgaaataaa tatagaaaag agggcatccc ccagccccac agcacaagac cctggccctc agcgctggac agetgagaca gaegeagget egetgeteag ggggagtaag tgetgggete eagtaggete ccacaggccc actgaggcag aggcatgagt cgcccaagtg ctggatgggg catggggaga aaggggcgtg ggcagccctg ctactgctgg caagaggtgg ccccattttt tccagatggg gaaactgagg cacaaggagg tttgggaact tgcccaaggt cactcacagt gagtcagctt tttaggggga ggagagegge teacaetetg ggaaacacag teaceteece aetggggage agggccaggc aggaggggcc tcagggccca tgactgcctg gaggggacac tcagcctctc tgaggacata tggggggtag gcctctgggg aagggtcttt gcttggcatc aggcagggcc aagtccagta agggcaaggg gagggggcat tctggtgaga acagcatttc tggcaagacg ggcatccact tcaaaatctc qgctcaaaag ggcagcaggg ctgttctcaa gccaggcagg 1080

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        35
Ser Arg Ala Val Leu Lys Pro Gly Arg Gln Gly Pro Pro Ile Pro Thr
                                             60
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Ile Leu Leu Ser Pro Ser Pro Pro Trp Arg Thr Leu Ala Arg Val Tyr
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pro Thr Ile Pro
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 240
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Glu Ala Thr Leu Gly Ser Gly Asn Leu Arg Gln Ala Val Met Leu Pro
                            40
Glu Gly Glu Asp Leu Asn Glu Trp Ile Ala Val Asn Thr Val Asp Phe
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Phe Asn Gln Ile Asn Met Leu Tyr Gly Thr Ile Thr Glu Phe Cys Thr
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Glu Ala Ser Cys Pro Val Met Ser Ala Gly Pro Arg Tyr Glu Tyr His
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Trp Ala Asp Gly Thr Asn Ile Lys Lys Pro Ile Lys Cys Ser Ala Pro
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            100
Lys Tyr Ile Asp Tyr Leu Met Thr Trp Val Gln Asp Gln Leu Asp Asp
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Glu Thr Leu Phe Pro Ser Lys Ile Gly Val Pro Phe Pro Lys Asn Phe
                                            140
                        135
Met Ser Val Ala Lys Thr Ile Leu Lys Arg Leu Phe Arg Val Tyr Ala
                                        155
                    150
His Ile Tyr His Gln His Phe Asp Ser Val Met Gln Leu Gln Glu Glu
                                    170
                165
Ala His Leu Asn Thr Ser Phe Lys His Phe Ile Phe Phe Val Gln Glu
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Phe Asn Leu Ile Asp Arg Arg Glu Leu Ala Pro Leu Gln Glu Leu Ile
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Glu Lys Leu Gly Ser Lys Asp Arg
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His Pro Arq Val Val Glu Leu Pro Lys Thr Asp Glu Gly Leu Gly Phe
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Asn Ile Met Gly Gly Lys Glu Gln Asn Ser Pro Ile Tyr Ile Ser Arg
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Val Ile Pro Gly Gly Val Ala Asp Arg His Gly Gly Leu Lys Arg Gly
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Asp Gln Leu Leu Ser Val Asn Gly Val Ser Val Glu Gly Glu Gln His
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Glu Lys Ala Val Glu Leu Leu Lys Ala Ala Gln Gly Ser Val Lys Leu
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Val Val Arg Tyr Thr Pro Arg Val Leu Glu Glu Met Glu Ala Arg Phe
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Glu Lys Met Arg Ser Ala Arg Arg Gln Gln His Gln Ser Tyr Ser
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Ser Leu Glu Ser Arg Gly
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180
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Asn Gln Gln Pro Ala Ala Pro Glu Cys Lys Val Leu Thr Ala Ala Gly
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Arg Val Lys Ala Lys Gln Lys Pro Leu Ile Ser Asn Ser His Thr Asp
                         55
His Leu Met Gly Cys Thr Lys Ser Ala Glu Pro Gly Thr Glu Thr Ser
                                         75
Gln Val Asn Ser Phe Ser Asp Leu Lys Ala Ser Thr Leu Val His Lys
                                     90
 Pro Gln Ser Asp Phe Thr Asn Asp Ala Leu Ser Pro Lys Phe Asn Leu
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             100
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Lys Cys Asn Glu Ile Glu Ser His Ile Ile Lys Gln Glu Asp Ile Leu
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Arg Cys Trp Thr Arg Ser Ile Arg Lys Pro Gln Gly His Val Arg Pro
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Cys Leu Val Gly Thr Thr Ala Ser Phe Gly Tyr Leu Ile Pro Ser Tyr
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Val Leu Met Glu Leu Glu Lys Pro Val Leu Ile Ser Leu Gly Lys Gly
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Met Lys Ala Leu Glu Tyr Ala Cys Gly Ile Lys Ala Glu Val Val Gly
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Lys Pro Ser Pro Glu Phe Phe Lys Ser Ala Leu Gln Ala Ile Gly Val
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Trp His Pro Arg Ser Arg Asp Val Ala Gln Leu Gly Asp Val Val His
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Glu Val Lys Gly Glu Ile Ala Arg Lys Asp Glu Lys Leu Leu Ser Phe
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Lys Asp His His Phe Asp Met Ile Asn Ile Lys Ser Ile Pro Lys Gly
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What is claimed is:

1. An isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is any integer 1-3161, or the complement thereof.

- 2. The isolated nucleic acid molecule of claim 1, said molecule hybridizing under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule comprising the sequence of nucleotides selected from the group consisting of SEQ ID NO:2n-wherein n is any integer 1-3161, or the complement thereof.
- 3. The isolated nucleic acid molecule of claim 1, said molecule encoding a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ II NO: 2n, wherein n is any integer 1-3161, or an amino acid sequence comprising one or more conservative substitutions in the amino acid sequence selected from the group consisting of SI ID NO: 2n.
- 4. The isolated nucleic acid molecule of claim 1, wherein said molecule encodes: polypeptide comprising the amino acid sequence selected from the group consisting of SEQ II NO: 2n, wherein n is any integer 1-3161.
- 5. The isolated nucleic acid molecule of claim 1, wherein said molecule comprise the sequence of nucleotides selected from the group consisting of SEQ ID NO:2*n*-1, wherein *i* any integer 1-3161, or the complement thereof.
- 6. An oligonucleotide less than 100 nucleotides in length and comprising at least contiguous nucleotides selected from the group consisting of SEQ ID NO:2n-1, wherein n is a integer 1-3161, or the complement thereof.
 - 7. A vector comprising the nucleic acid molecule of claim 1.

- 8. The vector of claim 7, wherein said vector is an expression vector.
- 9 A host cell comprising the isolated nucleic acid molecule of claim 1.
- 10. A substantially purified polypeptide comprising an amino acid sequence at least 80% identical to a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is any integer 1-3161.
- 11. The polypeptide of claim 10, wherein said polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is any integer 1-3161.
 - 12. An antibody that selectively binds to the polypeptide of claim 10.
- 13. A pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a therapeutic selected from the group consisting of:
 - a) the nucleic acid of claim 1;
 - b) the polypeptide of claim 10; and
 - c) the antibody of claim 12; and a pharmaceutically acceptable carrier.
- 14. A kit comprising in one or more containers, a therapeutically or prophylactically effective amount of the pharmaceutical composition of claim 13.
- 15. A method of producing the polypeptide of claim 10, said method comprising culturing the host cell of claim 9 under conditions in which the nucleic acid molecule is expressed.
- 16. A method of detecting the presence of the polypeptide of claim 10 in a sample, comprising contacting the sample with a compound that selectively binds to said polypeptide under conditions allowing the formation of a complex between said polypeptide and said

compound, and detecting said complex, if present, thereby identifying said polypeptide in said sample.

- 17. A method of detecting the presence of a nucleic acid molecule of claim 1 in a sample, the method comprising contacting the sample with a nucleic acid probe or primer that selectively binds to the nucleic acid molecule and determining whether the nucleic acid probe of primer bound to the nucleic acid molecule of claim 1 is present in the sample.
- 18. A method for modulating the activity of the polypeptide of claim 10, the method comprising contacting a cell sample comprising the polypeptide of claim 10 with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptid
- 19. The use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a ORFX-associated disorder, wherein said therapeutic is selected fro the group consisting of:
 - a) the nucleic acid of claim 1;
 - b) the polypeptide of claim 10; and
 - c) the antibody of claim 12.
- 20. A method for screening for a modulator of activity or of latency or predispositio to an ORFX-associated disorder, said method comprising:
 - a) contacting a test compound with the polypeptide of claim 10; and
- b) determining if said test compound binds to said polypeptide, wherein binding of said test compound to said polypeptide indicates the test compound is a modulator of activity or of latency or predisposition to an ORFX-associated disorder.
- 21. A method for screening for a modulator of activity or of latency or predisposition to an ORFX-associated disorder, said method comprising:
 - administering a test compound to a test subject at an increased risk ORFXassociated disorder, wherein said test subject recombinantly expresses a polypeptide encoded by the nucleotide of claim 1;

- b) measuring expression the activity of said protein in said test subject;
- measuring the activity of said protein in a control subject that recombinantly expresses said protein and is not at increased risk for an ORFX-associated disorder; and
- d) comparing expression of said protein in said test subject and said control subject, wherein a change in the activity of said protein in said test subject relative to said control subject indicates the test compound is a modulator or of latency of predispostition to an ORFX-associated disorder.
- 22. The method of claim 20, wherein said test animal is a recombinant test animal that expresses a test protein transgene or expresses said transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein said promoter is not the native gene promoter of said transgene.
- 23. A method for determining the presence of or predisposition to a disease associated with altered levels of a polypeptide of claim 11 in a subject, the method comprising:
 - a) measuring the amount of the polypeptide in a sample from said subject; and
 - comparing the amount of said polypeptide in step (a) to the amount of the polypeptide present in a control sample,

wherein an alteration in the level of the polypeptide in step (a) as compared to the control sample indicates the presence of or predisposition to a disease in said subject.

- 24. The method of claim 23, wherein said subject is a human.
- 25. A method for determining the presence of or predisposition to a disease associated with altered levels the nucleic acid molecule of claim 1 in a subject, the method comprising:
 - a) measuring the amount of the nucleic acid in a sample from the mammalian subject; and
 - b) comparing the amount of said nucleic acid in step (a) to the amount of the nucleic acid present in a control sample,

wherein an alteration in the level of the nucleic acid in step (a) as compared to the corsample indicates the presence of or predisposition to said disease in said subject.

- 26. The method of claim 25, wherein said subject is a human.
- 27. A method of treating or preventing a pathological condition associated with at ORFX-associated disorder in a subject, the method comprising administering to said subject polypeptide of claim 10 in an amount sufficient to alleviate or prevent said pathological condition.
 - 28. The method of claim 27, wherein said subject is a human.
- 29. A method of treating or preventing a pathological condition associated with at ORFX-associated disorder in a subject, the method comprising administering to said subject nucleic acid molecule of claim 1 in an amount sufficient to alleviate or prevent said pathological condition.
 - 30. The method of claim 29, wherein said subject is a human.
- 31. A method of treating or preventing a pathological condition associated with ar ORFX-associated disorder in a subject, the method comprising administering to said subject 1 antibody of claim 12 in an amount sufficient to alleviate or prevent said pathological conditio
 - 32. The method of claim 31, wherein said subject is a human.

(19) World Intellectual Property Organization International Bureau



(43) International Publication Date 5 October 2000 (05.10.2000)

(10) International Publication Number WO 00/58473 A3

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- Richard, A. [US/US]; 191 Leete Street, West Haven, CT 06516 (US). LEACH, Martin [GB/US]; 884 School Street, Webster, MA 01570 (US).
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- (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).
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(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US 60/127,607 (CIP) Filed on 31 March 1999 (31.03.1999) US 60/127,636 (CIP) Filed on 2 April 1999 (02.04.1999) US 60/127,728 (CIP) Filed on 5 April 1999 (05.04.1999) US 09/540,763 (CIP) Filed on 30 March 2000 (30.03.2000)

Published:

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UG, US, UZ, VN, YU, ZA, ZW.

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- (71) Applicant (for all designated States except US): CURA-GEN CORPORATION [US/US]; 555 Long Wharf Drive, 11th Floor, New Haven, CT 06511 (US).
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(72) Inventors; and

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- (75) Inventors/Applicants (for US only): SHIMKETS,

(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"

(57) Abstract: The present invention provides open reading frames encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.

INTERNATIONAL SEARCH REPORT

Internat Application No PCT/US 00/08621

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A CLASS	SIFICATION OF SUBJECT MATTER C12N15/12 C07K14/47 C07 C12N15/11 C12N15/62 A01	7K16/18 LK67/027	G01N33/566 A61K38/00	C12Q1/68
According	to International Patent Classification (IPC) or to both national	classification and	IPC	
	SEARCHED			
Minimum d IPC 7	ocumentation searched (classification system followed by cl C12N C07K G01N A01K A61K	assification symbo	ols)	
	tion searched other than minimum documentation to the exte			
	data base consulted during the international search (name of		•	
C. DOCUM	ENTS CONSIDERED TO BE RELEVANT			
Category *	Citation of document, with indication, where appropriate, or	f the relevant pass	sages	Relevant to claim No.
A	COLE S.T.: "Deciphering the Mycobacterium tuberculosis for complete genome sequence." NATURE, vol. 393, 11 June 1998 (1998-XP002144873) sequence LAMERDIN J.E.: "Sequence and 3.5 Mb contig in human 19p13. a serine protease gene cluste EMEST DATABASE ENTRY, 8 February 1999 (1999-02-08) sequence	rom the -06-11), alysis of 3 contair	a ii ng	
X Furthe	er documents are listed in the continuation of box C.	P	atent family members an	e listed in annex.
Special cate	gories of cited documents :	T later d	or most mublished of	the international files dec
'A" documen conside	t defining the general state of the art which is not red to be of particular relevance	or pri	ority date and not in confl to understand the princip	the international filing date lict with the application but le or theory underlying the
filling dat		"X" docum	ent of particular relevance	e; the claimed invention cannot be considered to
WITICH IS	t which may throw doubts on priority claim(s) or cited to establish the publication date of another	involv	e an inventive step when ent of particular relevance	the document is taken alone
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other me P" document later that	eans t published prior to the international filing date but n the priority date claimed	ments in the	i, such combination being	g obvious to a person skilled
	tual completion of the international search		f mailing of the internation	
	August 2000			3.11.00
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	European Patent Office, P.B. 5818 Patentiaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nt, Fax: (+31-70) 340-3016	}	lix, R	

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		PCT/US 00/08621
	ation) DOCUMENTS CONSIDERED TO BE RELEVANT	
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	M.D. ADAMS ET AL.: "The genome sequence of Drosophila melanogaster." SCIENCE, vol. 287, 24 March 2000 (2000-03-24), pages 2185-2195, XP002144875 the whole document	6

INTERNATIONAL SEARCH REPORT

inte ional application No. PCT/US 00/08621

Box I	Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)	
This Inte	ernational Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:	
1. X	Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:	
	Although claims 27 to 32 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.	
2.	Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:	
	Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).	
Box II	Observations where unity of invention is lacking (Continuation of item 2 of first sheet)	_
This Inter	national Searching Authority found multiple inventions in this international application, as follows:	_
	see additional sheet	
1.	As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.	
2. A	as all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment fany additional fee.	
3. A	s only some of the required additional search fees were timely paid by the applicant, this International Search Report overs only those claims for which fees were paid, specifically claims Nos.:	
	o required additional search fees were timely paid by the applicant. Consequently, this International Search Report is stricted to the invention first mentioned in the claims; it is covered by claims Nos.: Laims 1 to 32 partially	
Remark on	The desired as the desired as the desired by the applicant's profess.	
	No protest accompanied the payment of additional search fees.	

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claim: 1 to 32 partially

Isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from a group consisting of SEQ ID NO 2n wherein n is 1, oligonucleotides less than 100 nucleotides in length and comprising at least 6 contiguous nucleotides from the above sequence, polypeptides encoded by said nucleotides, antibodies that bind to said polypeptide, pharmaceutical composition comprising said polypeptide and methods of detection, screening, therapeutic uses involving said polypeptide.

2. Claim : .

Inventions 2 to 3161

claims 1 to 32 partially:

Isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from a group consisting of SEQ ID NO 2n wherein n is 2 to 3161, oligonucleotides less than 100 nucleotides in length and comprising at least 6 contiguous nucleotides from the above sequence, polypeptides encoded by said nucleotides, antibodies that bind to said polypeptide, pharmaceutical composition comprising said polypeptide and methods of detection, screening, therapeutic uses involving said polypeptide.